Increasing female age also affected the rates and locations of sperm depletion. This study provides direct evidence that females influence sperm fate by regulating sperm depletion and that this influence is affected by both somatic condition and environment.

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Program/Abstract # 350
Testes specific neurotransmitter transporter essential for male fertility in *Drosophila melanogaster*
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The predicted protein sequence for Neurotransmitter transporter like (Ntl) or CG7075 in *Drosophila*, shares a very strong homology with members of the sodium dependent neurotransmitter transporter family. Ntl expression is restricted to the male germline. Mobilization of a P element inserted in the 3′ end of the gene yields male sterile mutants defining a single complementation group. The mutant phenotype is completely rescued by germline transformation with Ntl cDNA under a testis specific promoter, also Ntl genomic DNA under it's native promoter. EM cross-sections show mutant cysts undergo normal individualization. Mutants counterstained using TRITC-phalloidin in don-juan and β-tubulin GFP background demonstrates perfect formation of actin cones around the axoneme and movement of the individualization complex along the length of the cyst. Individualized sperms in the mutants undergo coiling however they are not transferred into seminal vesicles and are immotile. To localize Ntl, an EGFP–Ntl fusion under a testis specific promoter was constructed. Germline transformation of the construct completely rescued the mutant phenotype. Initial studies suggest localization in intra cellular organelles, which is very unusual for a member of the SLC6a family. Sequence alignments of ntl with other SLC6a transporters suggest glycine as a likely substrate. One model currently being explored is that Ntl functions as a glycine transporter in the testes to provide the large amount of glycine required for polyglycylation of axonemal tubulins required in sperm maturation and motility (Rogowski et al., 2008).

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Program/Abstract # 351
Closing ring channels in the *C. elegans* gonad
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A fully-grown *C. elegans* oocyte is a large cell, the size of the 558 cells it will generate during embryogenesis. Most of the growth of the oocyte occurs during stages when its nucleus is transcriptionally quiescent. The distal region of the *C. elegans* gonad is a syncytium, with germ cells connected by ring channels. We determined that there is bulk streaming of the cytoplasmic materials in the core of the *C. elegans* gonad, and this streaming transfers material from a region of transcriptionally active pachytene-stage nuclei in the distal gonad into the proximal, enlarging, oocytes via ring channels. Since oocytes are uniform in size, and are ovulated every 23 min, there must be a cell size control mechanism. “Large oocyte mutants” have proximal oocytes that retain open ring channels for a prolonged period of time (Nadarajan et al., 2009). My aim is to better understand the mechanism that regulates ring channel closure. Actin and non-muscle myosin II (NMY-2) localize to ring channels. The closure of the ring channel is somewhat reminiscent of the actomyosin ring during cell division. However, midbody proteins are not localized, or at least not at significant levels, at ring channels. Using RNAi to knockdown actin-related proteins I will evaluate oocyte size, ring channel structure, actin and NMY-2 localization in the gonad. Furthermore, live-imaging will elucidate the progress of ring channel closure in manipulated animals. Data from these studies will provide a preliminary model for a cytoskeletal mechanism of ring channel closure.

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Program/Abstract # 352
Trans-generational epigenetic regulation in *C. elegans* primordial germ cells
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Epigenetic mechanisms are thought to help regulate the unique transcription program that is established in germ cell development and ensures germline continuity across generations. However, the mechanisms remain poorly understood. We show that a histone H3K36 methyltransferse, MES-4, is an epigenetic modifier that prevents aberrant transcription activity in *C. elegans* primordial germ cells (PGCs). In mes-4 mutants, RNA Pol II activation is abnormally regulated and the PGCs degenerate. Genetic and genome-wide analyses of MES-4-mediated H3K36 methylation suggest that MES-4 is predominantly responsible for maintenance, not de novo or transcription-coupled, methylation of H3K36. MES-4 appears to maintain an epigenetic memory of transcription occurring in germ cells of previous generations, and thus marks germline-expressed loci, probably to maintain their proper regulation as the genome is transferred across generations.

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Program/Abstract # 353
Dicer interacts with the P-granule component GLH-1 in *C. elegans*
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P granules, which are ribonuclear protein complexes specific to the outer, cytoplasmic side of the nuclear pores of *C. elegans* germ cells, are implicated in post-transcriptional control of maternally-transcribed mRNAs. Here we show a relationship in *C. elegans* between Dicer, the riboendonuclease processing enzyme of the RNA interference and microRNA pathways, and a constitutive component of P granules, the RNA helicase, GLH-1. Based on results from immuno-precipitations and GST-pull-downs, GLH-1 binds to DCR-1 and this binding does not require RNA. Both GLH-1 protein and mRNA levels are reduced in the dcr-1(ok247) null mutant background; conversely, a reduction of DCR-1 protein is observed in the glh-1(gk100) deletion strain. Thus, in the *C. elegans* germline, DCR-1 and GLH-1 demonstrate a germline-specific interdependence and both are necessary for the maintenance of the germline lineage. In addition, evidence indicates that levels of DCR-1 protein, like that of GLH-1, are regulated by proteosomal degradation, likely targeted by the Jun N-terminal kinase KGB-1. In adult germ cells DCR-1 is located in uniformly distributed small puncta throughout the cytoplasm, as well as being localized to the inner side of the nuclear pores, and to P granules. In arrested oocytes, GLH-1 and DCR-1 re-